Figure 4

A

```
FIX       176834-GTCTGCAACATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
RACE_95_3         GTCTGCAACATGCGGCTGTGTCTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
RACE_95_8         GTCTGCAACATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
RACE_95_11        GTCTGCAACATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG


FIX               GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAA--CGATTATTACCGAGTACCGCATTACT
RACE_95_3         GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAA--CGATTATTACCGAGTACCGCATTACT
RACE_95_8         GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAA--CGATTATTACCGAGTACCGCATTACT
RACE_95_11        GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAAAACGATTATTACCGAGTACCGCATTACT


FIX               GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG
RACE_95_3         GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG
RACE_95_8         GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG
RACE_95_11        GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG


FIX               TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGC
RACE_95_3         TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGC
RACE_95_8         TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGC
RACE_95_11        TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGC


FIX               TCAAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGT
RACE_95_3         TCAAGAG-------------------------------------------------------
RACE_95_8         TCAAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGT
RACE_95_11        TCAAGAG-------------------------------------------------------


FIX               AACGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTCGGAACCTGTGCTTGCAGAATCA
RACE_95_3         ----------------------------------------------------------AATCA
RACE_95_8         AACGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTCGGAACCTGTGCTTGCAGAATCA
RACE_95_11        ----------------------------------------------------------AATCA


FIX               ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCA
RACE_95_3         ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTATACGTCAGAACCGTCGCGGCGGCA
RACE_95_8         ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCA
RACE_95_11        ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCA


FIX               CCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCG
RACE_95_3         CCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCG
RACE_95_8         CCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCG
RACE_95_11        CCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCG


FIX               AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA-176346
RACE_95_3         AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA
RACE_95_8         AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA
RACE_95_11        AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA
```

B

```
FIX       175631-CCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG
RACE_95_3         CCGTGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG
RACE_95_8         CCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG
RACE_95_13        CCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG


FIX7              GGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC
RACE_95_3         GGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC
RACE_95_8         GGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC
RACE_95_11        GGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC


FIX               CACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTA
RACE_95_3         CACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTA
RACE_95_8         CACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTA
RACE_95_11        CACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGC-------
```

```
FIX             TTTTTATGATTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTGATAG
RACE_95_3       TTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGATAG
RACE_95_8       TTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGATAG
RACE_95_11      ------------------------------------------------------------


FIX             CCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTG
RACE_95_3       CCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTG
RACE_95_8       CCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTG
RACE_95_11      ------------------------------------------------------GCTG


FIX             CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGATC
RACE_95_3       CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGATC
RACE_95_8       CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGATC
RACE_95_11      CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGATC


FIX             GTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGC
RACE_95_3       GTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAACTGC
RACE_95_8       GTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGC
RACE_95_11      GTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGC


FIX             AACTACAATCCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACAGA
RACE_95_3       AACTACAATCC-----------------------------------------------
RACE_95_8       AACTACAATCC-----------------------------------------------
RACE_95_11      AACTACAATCT-----------------------------------------------


FIX             GGGACAAAACATCATTAAAAAAAAAGTCTAATTTCACGTTTTGTACCCCCCCTTCCCCTC
RACE_95_3       ------------------------------------------------------------
RACE_95_8       ------------------------------------------------------------
RACE_95_11      ------------------------------------------------------------


FIX             CGTGTTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA
RACE_95_3       ----------GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA
RACE_95_8       ----------GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA
RACE_95_11      ----------GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA


FIX             AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT
RACE_95_3       AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT
RACE_95_8       AGGCGCAGTACCTGCTGGGCGCCGCTGGCGGCGTTCCCTATCGATGGATCAACCTGGAAT
RACE_95_11      AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT

FIX             ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACA
RACE_95_3       ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACA
RACE_95_8       ACGACAAGATAGCCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACA
RACE_95_11      ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAATACA


FIX             AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA-174887
RACE_95_3       AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA----
RACE_95_8       AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA----
RACE_95_11      AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA----
```

C

```
FIX     174892-CGCTAAAATGGGCTATATGCTGCAGTGAATAAAAAATGTGTGTTTGTCCGA-174841
RACE_95_3    … CGCTAAAATGGGCTATATGCTGCAGTGAATAAAAAATGTGTGTTTGTCCGCAAAAAAAA …
RACE_95_8    … CGCTAAAATGGGCTATATGCTGCAGTGAATAAAAAATGTGTGTTTGTCCAAAAAAAAAA …
RACE_95_11   … CGCTAAAATGGGCTATATGCTGCAGTGAATAAAAAATGTGTGTTTGTCCAAAAAAAAAA …
```

Fig. 4 UL131-128 mRNA processing – Panels (**A-C**) compare FIX-BAC DNA sequence (numbered according to Chee et al.) to a set of cDNA sequences from RACE clones 95-3, 95-8 and 95-11 **(A)** UL131 region, **(B)** UL128 region, **(C)** UL131-128 transcripts 3´ end. Start codons, stop codons and the polyA site are in bold face, mRNA processing signals (splice donor sequence, splice acceptor sequence, AATAAA signal) are grey-shaded.

Figure 5

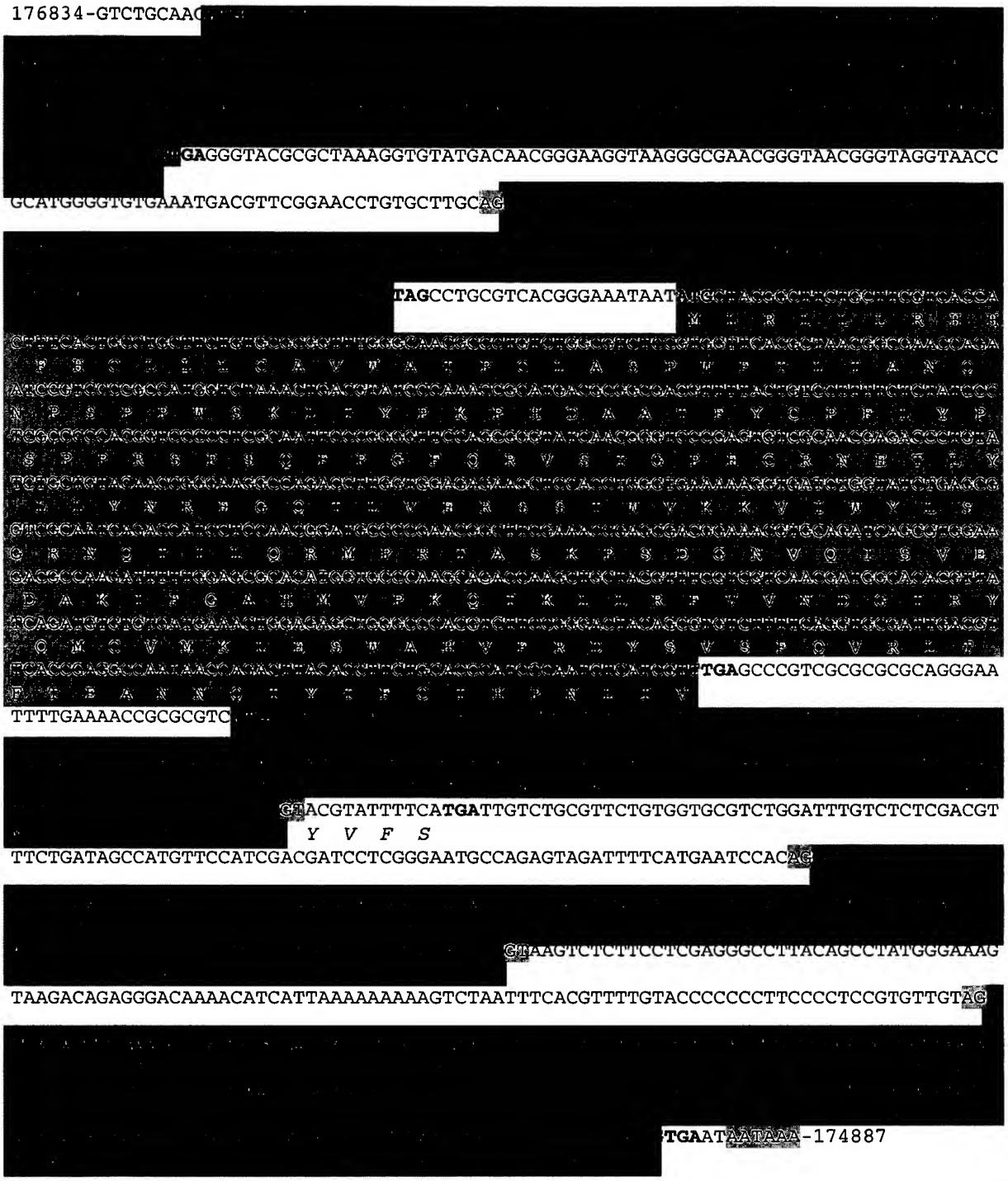


Fig. 5 Exon-intron organization of the FIX-BAC UL131-128 genetic locus. UL131 (green); UL130 (orange); UL128 (blue); UL128x1 C-terminus (light blue).

Figure 6

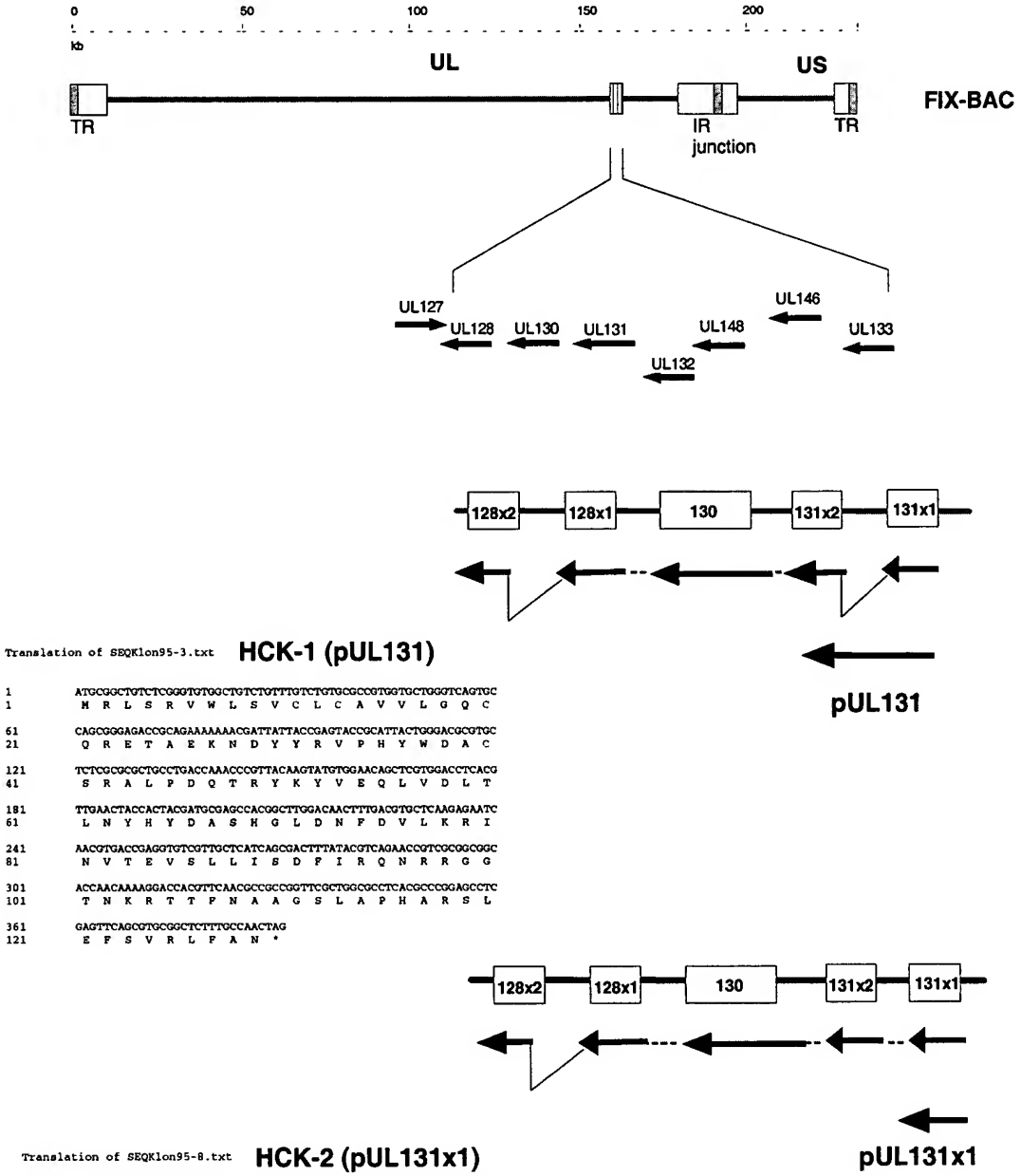
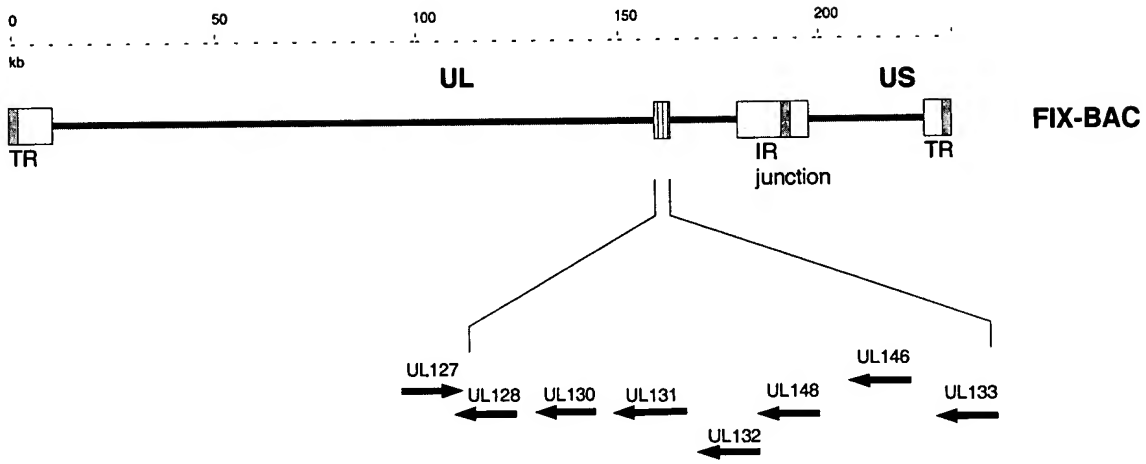


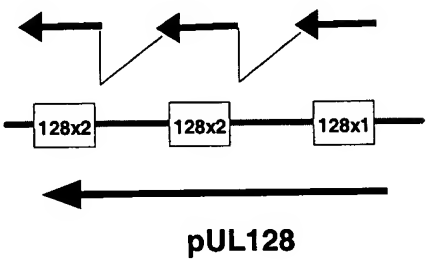
Fig. 6 Scheme of the differentially spliced transcripts of the UL131-128 region. Upper panel RACE clone 95-3 and predicted open reading frame (orf) pUL131 (HCK-1). Lower panel RACE clone 95-8 and predicted orf UL131x1 (HCK-2).

Figure 7



Translation of SEQ128.txt(1-563 : **HCK-4 (pUL128)**

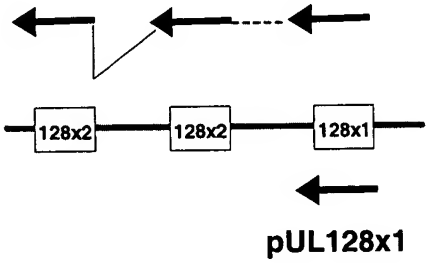
```
1        ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
1         M  S  P  K  N  L  T  P  F  L  T  A  L  W  L  L  L  G  H  S

61       CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
21        R  V  P  R  V  R  A  E  E  C  C  E  F  I  N  V  N  H  P  P

121      GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCACTGCGGTGTCCGGAC
41        E  R  C  Y  D  F  K  M  C  N  R  F  T  V  A  L  R  C  P  D

181      GGCGAAGTCTGCTACAGTCCCGAGAAACGGCTGAGATTCGCGGGATCGTCACCACCATG
61        G  E  V  C  Y  S  P  E  K  T  A  E  I  R  G  I  V  T  T  M

241      ACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAATCTG
81        T  H  S  L  T  R  Q  V  V  H  N  K  L  T  S  C  N  Y  N  L

301      TTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGTAC
101       L  Y  L  E  A  D  G  R  I  R  C  G  K  V  N  D  K  A  Q  Y

361      CTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGATA
121       L  L  G  A  A  G  S  V  P  Y  R  W  I  N  L  E  Y  D  K  I

421      ACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGGAT
141       T  R  I  V  G  L  D  Q  Y  L  E  S  V  K  K  H  K  R  L  D

481      GTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGA
161       V  C  R  A  K  M  G  Y  M  L  Q  *
```



pUL128

Translation of SEQ128 x 1txt **HCK-3 (pUL128x1)**

```
1        ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
1         M  S  P  K  N  L  T  P  F  L  T  A  L  W  L  L  L  G  H  S

61       CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
21        R  V  P  R  V  R  A  E  E  C  C  E  F  I  N  V  N  H  P  P

121      GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA
41        E  R  C  Y  D  F  K  M  C  N  R  F  T  V  A  Y  V  F  S  *
```



pUL128x1

Fig. 7 Scheme of the differentially spliced transcripts of the UL131-128 region. Upper panel SEQUL128B and predicted open reading frame (orf) pUL128 (HCK-4). Lower panel SEQUL128A and predicted orf UL128x1 (HCK-3).

Figure 8

Northern Blot Analys s

RVFIX, RVFIX mutants and laboratory strains:

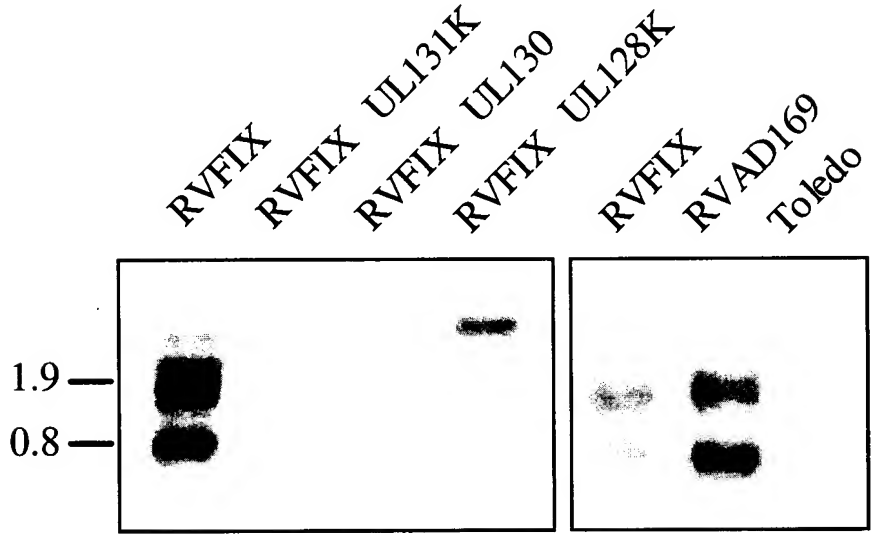


Fig. 8 mRNA was prepared from RVFIX-infected fibroblasts 4 days p.i. using Rneasy Mini, QIAshredder and Oligotex mRNA Mini kits according to the manufacturer's guidance (Qiagen). For Nothern blotting, 1 μg RNA was electrophoresed on an agarose gel according to the MOPS-formaldehyde protocol and blotted onto Hybond N+ membranes (Amersham Pharmacia). Blots were hybridized with a UL131-128 specific probe.

Figure 9

Comparison RACE clone 95-3 – FIX genomic sequence

Upper line: SEQFIX UL131-128.txt, from 10 to 1977
Lower line: SEQKlon95-3.txt, from 1 to 1741

```
SEQFIX UL131-128.txt:SEQKlon95-3.txt identity= 99.66%(1735/1741)
gap=11.94%(236/1977)

1      GTCTGCAACATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
                 |||||||||| ||||||||||||||||||||||||||||||||||||||||
1      .........ATGCGGCTGTCTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG

61     GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
52     GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGG

121    GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
112    GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG

181    GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGCTC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
172    GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGCTC

241    AAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGTAA
       |||||
232    AAGAG.....................................................

301    CGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTCGGAACCTGTGCTTGCAGAATCAAC
                                                             |||||||
235    ..........................................................AATCAAC

361    GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCACC
       |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
244    GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTATACGTCAGAACCGTCGCGGCGGCACC

421    AACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCGAG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
304    AACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCGAG

481    TTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
364    TTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC

541    TGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
424    TGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG

601    CGTCTCCGTGGTTCACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACTGA
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
484    CGTCTCCGTGGTTCACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACTGA

661    CGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTCTATCCCTCGCCCC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
544    CGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTCTATCCCTCGCCCC
```

```
721   CACGGTCCCCCTCGCAATTCCCGGGGTTCCAGCGGGTATCAACGGGTCCCGAGTGTCGCA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
604   CACGGTCCCCCTCGCAATTCCCGGGGTTCCAGCGGGTATCAACGGGTCCCGAGTGTCGCA

781   ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
664   ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA

841   CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACGGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
724   CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACGGA

901   TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAGACGCCA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
784   TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAGACGCCA

961   AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTCAACG
      |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
844   AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGCCAACG

1021  ATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCGGG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
904   ATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCGGG

1081  ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTCACCGAGGCCAATAACCAGACTTACA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
964   ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTCACCGAGGCCAATAACCAGACTTACA

1141  CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1024  CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA

1201  AACCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT
      ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
1084  AACCGTGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT

1261  TGGGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1144  TGGGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA

1321  ACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1204  ACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACG

1381  TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTGAT
      |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
1264  TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGAT

1441  AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1324  AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC

1501  TGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1384  TGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGA

1561  TCGTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCT
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
1444  TCGTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAACT

1621  GCAACTACAATCCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACA
      |||||||||||||
1504  GCAACTACAATCC.....................................................
```

```
1681  GAGGGACAAAACATCATTAAAAAAAAAGTCTAATTTCACGTTTTGTACCCCCCCTTCCCC

1517  ............................................................

1741  TCCGTGTTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA
                  ||||||||||||||||||||||||||||||||||||||||||||||||
1517  ............GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA

1801  CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1565  CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGA

1861  ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1625  ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA

1921  CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1685  CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA
```

Translation of SEQKlon95-3.txt: HCK-1 (pUL131)

```
1         ATGCGGCTGTCTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTGGGTCAGTGC
1          M  R  L  S  R  V  W  L  S  V  C  L  C  A  V  V  L  G  Q  C

61        CAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGGGACGCGTGC
21         Q  R  E  T  A  E  K  N  D  Y  Y  R  V  P  H  Y  W  D  A  C

121       TCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTGGACCTCACG
41         S  R  A  L  P  D  Q  T  R  Y  K  Y  V  E  Q  L  V  D  L  T

181       TTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGCTCAAGAGAATC
61         L  N  Y  H  Y  D  A  S  H  G  L  D  N  F  D  V  L  K  R  I

241       AACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTATACGTCAGAACCGTCGCGGCGGC
81         N  V  T  E  V  S  L  L  I  S  D  F  I  R  Q  N  R  R  G  G

301       ACCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTC
101        T  N  K  R  T  T  F  N  A  A  G  S  L  A  P  H  A  R  S  L

361       GAGTTCAGCGTGCGGCTCTTTGCCAACTAG
121        E  F  S  V  R  L  F  A  N  *
```

Figure 10

Comparison RACE clone 95-8 –FIX genomic sequence

Upper line: SEQFIX UL131-128.txt, from 10 to 1977
Lower line: SEQKlon95-8.txt, from 1 to 1849

```
SEQFIX UL131-128.txt:SEQKlon95-8.txt identity= 99.78%(1845/1849)
gap=6.47%(128/1977)


1      GTCTGCAACATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
1      .........ATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG

61     GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
52     GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGG

121    GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
112    GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG

181    GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGCTC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
172    GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGCTC

241    AAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGTAA
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
232    AAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGTAA

301    CGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTCGGAACCTGTGCTTGCAGAATCAAC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
292    CGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTCGGAACCTGTGCTTGCAGAATCAAC

361    GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCACC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
352    GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCACC

421    AACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCGAG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
412    AACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCGAG

481    TTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
472    TTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC

541    TGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
532    TGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG

601    CGTCTCCGTGGTTCACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACTGA
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
592    CGTCTCCGTGGTTCACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACTGA

661    CGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTCTATCCCTCGCCCC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
652    CGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTCTATCCCTCGCCCC
```

```
721   CACGGTCCCCCTCGCAATTCCCGGGGTTCCAGCGGGTATCAACGGGTCCCGAGTGTCGCA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
712   CACGGTCCCCCTCGCAATTCCCGGGGTTCCAGCGGGTATCAACGGGTCCCGAGTGTCGCA

781   ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
772   ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA

841   CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACGGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
832   CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACGGA

901   TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAGACGCCA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
892   TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAGACGCCA

961   AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTCAACG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
952   AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTCAACG

1021  ATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCGGG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1012  ATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCGGG

1081  ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTCACCGAGGCCAATAACCAGACTTACA
      |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
1072  ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTCACCGAGGCCGATAACCAGACTTACA

1141  CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1132  CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA

1201  AACCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1192  AACCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT

1261  TGGGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1252  TGGGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA

1321  ACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1312  ACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACG

1381  TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTGAT
      |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
1372  TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGAT

1441  AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1432  AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC

1501  TGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1492  TGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGA

1561  TCGTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1552  TCGTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCT

1621  GCAACTACAATCCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACA
      ||||||||||||
1612  GCAACTACAATCC............................................
```

```
1681  GAGGGACAAAACATCATTAAAAAAAAAGTCTAATTTCACGTTTTGTACCCCCCCTTCCCC

1625  ............................................................

1741  TCCGTGTTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA
                  ||||||||||||||||||||||||||||||||||||||||||||||||
1625  ............GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA

1801  CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGA
      |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
1673  CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCGGCGTTCCCTATCGATGGATCAACCTGGA

1861  ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA
      |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
1733  ATACGACAAGATAGCCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA

1921  CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1793  CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA
```

Translation of SEQKlon95-8.txt: HCK-2 (pUL131x1)

```
1          ATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTGGGTCAGTGC
1           M  R  L  C  R  V  W  L  S  V  C  L  C  A  V  V  L  G  Q  C

61         CAGCGGGAGACCGCAGAAAAAAACGATTATTACCGAGTACCGCATTACTGGGACGCGTGC
21          Q  R  E  T  A  E  K  N  D  Y  Y  R  V  P  H  Y  W  D  A  C

121        TCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTGGACCTCACG
41          S  R  A  L  P  D  Q  T  R  Y  K  Y  V  E  Q  L  V  D  L  T

181        TTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGCTCAAGAGGTGA
61          L  N  Y  H  Y  D  A  S  H  G  L  D  N  F  D  V  L  K  R  *
```

Figure 11

Comparison RACE clon 95-11 –FIX genomic sequenc

Upper line: SEQFIX UL131-128.txt, from 10 to 1977
Lower line: SEQKlon95-11.txt, from 1 to 1620

```
SEQFIX UL131-128.txt:SEQKlon95-11.txt identity= 99.57%(1611/1618)
gap=18.24%(361/1979)

1      GTCTGCAACATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1      .........ATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG

61     GGTCAGTGCCAGCGGGAGACCGCAG..AAAAAAACGATTATTACCGAGTACCGCATTACT
       |||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
52     GGTCAGTGCCAGCGGGAGACCGCAGAAAAAAAAAACGATTATTACCGAGTACCGCATTACT

119    GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
112    GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG

179    TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
172    TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACTTTGACGTGC

239    TCAAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGT
       |||||||
232    TCAAGAG.....................................................

299    AACGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTCGGAACCTGTGCTTGCAGAATCA
                                                                |||||
237    ..........................................................AATCA

359    ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCA
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
244    ACGTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCA

419    CCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
304    CCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCGGAGCCTCG

479    AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCT
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
364    AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCT

539    TCTGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCT
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
424    TCTGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCT

599    GGCGTCTCCGTGGTTCACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACT
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
484    GGCGTCTCCGTGGTTCACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACT

659    GACGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTCTATCCCTCGCC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
544    GACGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTCTATCCCTCGCC
```

```
719   CCCACGGTCCCCCTCGCAATTCCCGGGGTTCCAGCGGGTATCAACGGGTCCCGAGTGTCG
      |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
604   CCCACGGTCCCCCTCGCAATTCCCGGGGTTCCAGCGGGTATTAACGGGTCCCGAGTGTCG

779   CAACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTC
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
664   CAACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTC

839   CACCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACG
      |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
724   CACCTGGGTGAAAAAGGTGATCTGGCATCTGAGCGGTCGCAATCAGACCATCCTCCAACG

899   GATGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAGACGC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
784   GATGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGGAAGACGC

959   CAAGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTCAA
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
844   CAAGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGCCAA

1019  CGATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCG
      |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
904   CGATGGCACACGTTATTAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCG

1079  GGACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTCACCGAGGCCAATAACCAGACTTA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
964   GGACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTCACCGAGGCCAATAACCAGACTTA

1139  CACCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1024  CACCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTG

1199  AAAACCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1084  AAAACCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCT

1259  ATTGGGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1144  ATTGGGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGT

1319  CAACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1204  CAACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGC..

1379  CGTATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTG

1262  ..........

1439  ATAGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAG

1262  ..........

1499  GCTGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1262  ACTGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGG

1559  GATCGTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1321  GATCGTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAG

1619  CTGCAACTACAATCCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGA
      ||||||||||||||
1381  CTGCAACTACAATCT..............................................
```

```
1679  CAGAGGGACAAAACATCATTAAAAAAAAAGTCTAATTTCACGTTTTGTACCCCCCCTTCC

1396  ............................................................

1739  CCTCCGTGTTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAAC
                  ||||||||||||||||||||||||||||||||||||||||||||||||
1396  ..............GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAAC

1799  GACAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1442  GACAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTG

1859  GAATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1502  GAATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAA

1919  CACAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1562  TACAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA
```

Figure 12

Comparison SEQ 128 B - FIX genomic sequence

Upper line: FIX genomic sequence
Lower line: SEQ 128 B

```
5998  ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1     ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC

6058  CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61    CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG

6118  GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121   GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA

6178  TTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGATAGCCATGTTCC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181   TTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGATAGCCATGTTCC

6238  ATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTGCGGTGTCCG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241   ATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTGCGGTGTCCG

6298  GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGATCGTCACCACC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301   GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGATCGTCACCACC

6358  ATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAAT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361   ATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAAT

6418  CCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACAGAGGGACAAAA
      ||
421   CC..........................................................

6478  CATCATTAAAAAAAAAGTCTAATTTCACGTTTTGTACCCCCCCTTCCCCTCCGTGTTGTA

423   ............................................................

6538  GGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
423   .GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT

6598  ACCTGCTGGGCGCCGCTGGCGGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
482   ACCTGCTGGGCGCCGCTGGCGGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA

6658  TAGCCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
542   TAGCCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG
```

```
6718  ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTTGTCC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
602   ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTTGTCC

6778  GAAATACGCGTTTTGAGATTTCTG
       |||  |          | |
662   AAAAAAAAAAAAAAAAAAAAAAA
```

Translation of SEQ128 B x 1.txt: HCK-3 (pUL128x1)

```
1          ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
1           M  S  P  K  N  L  T  P  F  L  T  A  L  W  L  L  L  G  H  S

61         CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
21          R  V  P  R  V  R  A  E  E  C  C  E  F  I  N  V  N  H  P  P

121        GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA
41          E  R  C  Y  D  F  K  M  C  N  R  F  T  V  A  Y  V  F  S  *
```

Figure 13

Comparison SEQ 128 A - FIX genomic sequence

Upper line: FIX-BAC
Lower line: SEQ128 A

```
5998   ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1      ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC

6058   CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61     CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG

6118   GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTTATGA
       ||||||||||||||||||||||||||||||||||||||||
121    GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGC..............

6178   TTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTGATAGCCATGTTCC

166    ............................................................

6238   ATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTGCGGTGTCCG
                                                   ||||||||||||
166    ...............................................GCTGCGGTGTCCG

6298   GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGATCGTCACCACC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
178    GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTCGCGGGATCGTCACCACC

6358   ATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAAT
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
238    ATGACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAAT

6418   CCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACAGAGGGACAAAA
       ||
298    CC..........................................................

6478   CATCATTAAAAAAAAAGTCTAATTTCACGTTTTGTACCCCCCCTTCCCCTCCGTGTTGTA

300    ............................................................

6538   GGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
300    .GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT

6598   ACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
359    ACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA

6658   TAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
419    TAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG

6718   ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTTGTCC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
479    ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTG
```

Translation of SEQ128 A: HCK-4 (pUL128)

```
1          ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
1           M  S  P  K  N  L  T  P  F  L  T  A  L  W  L  L  L  G  H  S

61         CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
21          R  V  P  R  V  R  A  E  E  C  C  E  F  I  N  V  N  H  P  P

121        GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCACTGCGGTGTCCGGAC
41          E  R  C  Y  D  F  K  M  C  N  R  F  T  V  A  L  R  C  P  D

181        GGCGAAGTCTGCTACAGTCCCGAGAAACGGCTGAGATTCGCGGGATCGTCACCACCATG
61          G  E  V  C  Y  S  P  E  K  T  A  E  I  R  G  I  V  T  T  M

241        ACCCATTCATTGACACGCCAGGTCGTACACAACAAACTGACGAGCTGCAACTACAATCTG
81          T  H  S  L  T  R  Q  V  V  H  N  K  L  T  S  C  N  Y  N  L

301        TTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGTAC
101         L  Y  L  E  A  D  G  R  I  R  C  G  K  V  N  D  K  A  Q  Y

361        CTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGATA
121         L  L  G  A  A  G  S  V  P  Y  R  W  I  N  L  E  Y  D  K  I

421        ACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGGAT
141         T  R  I  V  G  L  D  Q  Y  L  E  S  V  K  K  H  K  R  L  D

481        GTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGA
161         V  C  R  A  K  M  G  Y  M  L  Q  *
```

Figure 14

Translation of SEQUL130: HCK-5 (pUL130)

```
1          ATGCTACGGCTTCTGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCA
1           M  L  R  L  L  L  R  H  H  F  H  C  L  L  L  C  A  V  W  A

61         ACGCCCTGTCTGGCGTCTCCGTGGTTCACGCTAACGGCGAACCAGAATCCGTCCCCGCCA
21          T  P  C  L  A  S  P  W  F  T  L  T  A  N  Q  N  P  S  P  P

121        TGGTCTAAACTGACGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTC
41          W  S  K  L  T  Y  P  K  P  H  D  A  A  T  F  Y  C  P  F  L

181        TATCCCTCGCCCCCACGGTCCCCCTCGCAATTCCCGGGGGTTCCAGCGGGTATCAACGGGT
61          Y  P  S  P  P  R  S  P  S  Q  F  P  G  F  Q  R  V  S  T  G

241        CCCGAGTGTCGCAACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTG
81          P  E  C  R  N  E  T  L  Y  L  L  Y  N  R  E  G  Q  T  L  V

301        GAGAGAAGCTCCACCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACC
101         E  R  S  S  T  W  V  K  K  V  I  W  Y  L  S  G  R  N  Q  T

361        ATCCTCCAACGGATGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGC
121         I  L  Q  R  M  P  R  T  A  S  K  P  S  D  G  N  V  Q  I  S

421        GTGGAAGACGCCAAGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGT
141         V  E  D  A  K  I  F  G  A  H  M  V  P  K  Q  T  K  L  L  R

481        TTCGTCGTCAACGATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCC
161         F  V  V  N  D  G  T  R  Y  Q  M  C  V  M  K  L  E  S  W  A

541        CACGTCTTCCGGGACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTCACCGAGGCCAAT
181         H  V  F  R  D  Y  S  V  S  F  Q  V  R  L  T  F  T  E  A  N

601        AACCAGACTTACACCTTCTGCACCCATCCCAATCTCATCGTTTGA
201         N  Q  T  Y  T  F  C  T  H  P  N  L  I  V  *
```